

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2002, 07:40:45 ; Search time 37.8 Seconds

(without alignments)
4205.862 Million cell updates/sec

Title: US-08-153-397a-2
Perfect score: 4928

Sequence: 1 MGPEALSSLLLLLVASGDA.....QRPFSQHLRLADALNTV 919

Scoring table: BIOSIM62
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriapi:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4534	92.0	911	11	035407 mus musculus
2	2387	48.4	840	11	099P57 cricetus
3	1159	23.5	220	11	064108 rattus sp.
4	1044	21.2	797	5	0952V7 caenorhabd
5	1023	20.8	767	5	0952V6 caenorhabd
6	929.5	18.9	183	11	064107 rattus sp.
7	691	14.0	700	5	018433 geodia cydo
8	648	13.1	1145	5	09BK18 aplysia cal
9	633	12.8	811	13	09YH43 xenopus lae
10	631	12.8	821	13	09YH44 xenopus lae
11	628.5	12.7	486	13	09PST9 xenopus lae
12	623.5	12.7	780	13	090699 gallus gall
13	623.5	12.7	699	5	027656 geodia cydo
14	615	12.5	839	4	075682 homo sapien
15	615	12.5	503	4	015655 homo sapien
16	614	12.5	591	4	015656 homo sapien

17	611	12.4	767	5	018163 caenorhabd
18	608	12.3	282	13	091373 xenopus. tr
19	608	12.3	902	5	017576 caenorhabd
20	608	12.3	928	5	09B1X1 caenorhabd
21	597.5	12.1	946	13	007153 torpedo cal
22	593.5	12.0	868	11	062838 rattus norv
23	590	12.0	868	11	061006 mus musculu
24	590	12.0	871	11	061987 mus musculu
25	588.5	11.9	869	4	015146 homo sapien
26	588.5	11.9	881	11	061988 mus musculu
27	587.5	11.9	860	11	061005 mus musculu
28	584	11.9	685	5	024488 drosophila
29	576	11.7	981	15	092809 abelson mur
30	574	11.6	168	11	092209 caenorhabd
31	571	11.6	737	5	017305 xenopus lae
32	552	11.2	354	13	09DDA2 gallus gall
33	548	11.1	989	13	09PMW6 scophthalmu
34	541.5	11.0	1245	13	03YGH8 drosophila
35	538.5	10.9	724	5	09V6K3 xenopus lae
36	529	10.7	1362	13	09PVZ4 xenopus lae
37	523	10.6	1504	5	09YV86 drosophila
38	522.5	10.6	2317	11	063130 rattus norv
39	522.5	10.6	2338	11	063132 rattus norv
40	522	10.6	984	4	043718 homo sapien
41	521	10.6	1358	13	073798 xenopus lae
42	520	10.6	818	15	09PWS3 abelson mur
43	518	10.5	2340	11	064736 mus musculu
44	515	10.5	1418	13	093457 scophthalmu
45	512.5	10.4	863	5	076148 anopheles s

ALIGNMENTS

RESULT 1
035407 PRELIMINARY; PRT; 911 AA.
AC 035407;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RECEPTOR-LIKE TYROSINE KINASE.
GN NEP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=93390947; PubMed=8397369;
RA Zerlin M., Julius M.A., Goldfarb M.;
RT "NEP: a novel receptor-like tyrosine kinase expressed in proliferating neuroepithelia.";
RL Oncogene 8:2731-2739(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Zerlin M., Julius M.A., Goldfarb M.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
DR EMBL: AF062599; AAB81866.1; -.
DR HSPB; P00523; 2PTK.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR000421; FAS58_C.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF00754; F5_P8-type_C; 1.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00231; FAS58C; 1.

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DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS01285; FA58c_1; 1.
DR PROSITE; PS01286; FA58c_2; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
DR ATP-binding; Glycoprotein; kinase; phosphorylation; Receptor;
KW Transferrase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 911 AA; 101091 MW; D52EC50267D8014D CRC64;

1 Query Match 92.0%; Score 4534; DB 11; Length 911;
Best Local Similarity 92.3%; Pred. No. 0;
Matches 850; Conservative 21; Mismatches 38; Indels 12; Gaps 4;

QY 1 MGPEALSS-LILLVLVSGDAMKQAFDPKACRYALGMODRTIPDSISASSSSSDSTA 59
Db 1 MGTGLSSLLLLLVITGDDMGHFDPAKCRYALGMODRTIPDSISASSSSSDSTA 60
QY 60 RHRLESDDGAMCPAGSVPEKEEYLOVDLQRLHLVALVGTGRRHAGLGKEFSRSYR 119
Db 61 RHRLESDDGAMCPAGSVPEKEEYLOVDLQRLHLVALVGTGRRHAGLGKEFSRSYR 120
QY 120 LRYRSDGRHMGKDRNGOEYISGNEDEPGVYLKDLGPPVYARLVRFYPRADRYMSYCLR 179
Db 121 LRYRSDGRHMGKDRNGOEYISGNEDEPGVYLKDLGPPVYARLVRFYPRADRYMSYCLR 180
QY 180 VELGGLMRDGLSTYTPVGTGTYLSEA-VYINDSTYDGHVVGGLQYGGGLADGVVGL 238
Db 181 VELGGLMRDGLSTYTPVGTGTYLSEA-VYINDSTYDGHVVGGLQYGGGLADGVVGL 240
QY 239 DDFRKSQELRWPGYDYVYGSNSHSFSSGYVEMEFEFRLRAFMQVHCNMHTLGARLP 298
Db 241 DDFRKSQELRWPGYDYVYGSNSHSFSSGYVEMEFEFRLRAFMQVHCNMHTLGARLP 300
QY 299 GGVCCRRRRCGPAMAMEBEPKRNHNLGNLGDPRANAVSVPJGGRVAFRLQCRFLFAGFWLL 358
Db 301 GGVCCRRRRCGPAMAMEBEPKRNHNLGNLGDPRANAVSVPJGGRVAFRLQCRFLFAGFWLL 360
QY 359 FSEISFISDVYNNSSPALGFFPPAPMPMPPTNSSLLEPRGGOOPAKAGSPTAI 418
Db 361 FSEISFISDVYNNSSPALGFFPPAPMPMPPTNSSLLEPRGGOOPAKAGSPTAI 416
QY 419 LIGGLVAIIILLLLIILALMLRLMRRLLSKAERVLVEELTVHLSVPGDTILINRPGP 478
Db 417 LIGGLVAIIILLLLIILALMLRLMRRLLSKAERVLVEELTVHLSVPGDTILINRPGP 476
QY 479 REPPYDEPRRGRNPPHSAPCVYNGSALLSNPAYRLLIATYARPPGPGPTPAMAKPT 538
Db 477 REPPYDEPRRGRNPPHSAPCVYNGSALLSNPAYRLLIATYARPPGPGPTPAMAKPT 536
QY 539 NTOAYSGDYMEPEKAPALPPPPONSVPHYAEADIVTLQGVGNTYAVPALPGAVGD 598
Db 537 NTOAYSGDYMEPEKAPALPPPPONSVPHYAEADIVTLQGVGNTYAVPALPGAVGD 596
QY 599 GPPRVDEPRSRRLRKEKLGEGQFGEVHLCEVSPQDLVSLDFPLNVKRGHLLVAVKILR 658
Db 597 GPPRVDEPRSRRLRKEKLGEGQFGEVHLCEVSPQDLVSLDFPLNVKRGHLLVAVKILR 656
QY 659 PDAKKNASFLSFRNDLKEVKIKSLKADPNIIIRLLGVYQVDDPLCITITTMENGDINOF 718
Db 657 PDAKKNASFLSFRNDLKEVKIKSLKADPNIIIRLLGVYQVDDPLCITITTMENGDINOF 710
QY 719 LSAHOLEDKAEGAPGGQAAOGPTISYPMILHYAAQIASGMRYLATLVNVRDLATRNC 778
Db 711 LSAHOLEDKAEGAPGGQAAOGPTISYPMILHYAAQIASGMRYLATLVNVRDLATRNC 770
QY 779 LVGENFTIKIADFGMSNLYAGDIYRVQGRAVYPIRMAMCECILMGFTTASDVMAEGVT 838
Db 771 LVGENFTIKIADFGMSNLYAGDIYRVQGRAVYPIRMAMCECILMGFTTASDVMAEGVT 830
QY 839 LMEVLMCRSQPFGQLTDEQYIENAGEFFRDGQROYLSRPPACQRTLYELMLRCMSRES 898
Db 831 LMEVLMCRSQPFGQLTDEQYIENAGEFFRDGQROYLSRPPACQRTLYELMLRCMSRES 890
QY 899 EQRPPEFQALHREFLADALNTV 919
Db 891 EQRPPEFQALHREFLADALNTV 911

RESULT 2
ID Q99P57 PRELIMINARY; PRT; 840 AA.
AC Q99P57;
DE 01-JUN-2001 (TREMBLE). 17, Created
DE 01-JUN-2001 (TREMBLE). 17, Last sequence update
DE 01-DEC-2001 (TREMBLE). 19, Last annotation update
DE DISCOWDIN-1 DOMAIN RECEPTOR-2 (FRAGMENT).
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_Taxid=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Gerhardt C.C., Guillaume J.L., Strosberg A.D.;
RT "Activation of the endogenous collagen receptor DDR2 by cAMP/PKA and
RT cellular detachment in CHO/K1 cells."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
DR EMBL; AF329455; AAK01238.1; -.
DR HSSP; P06213; 1IRK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000421; FA58c.
DR InterPro; IPR002011; Receptor_tyr_kin_II.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase.1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00231; FA58c.1.
DR SMART; SM00220; S_TKc.1.
DR SMART; SM00219; TYKc.1.
DR PROSITE; PS01285; FA58c_1; 1.
DR PROSITE; PS01286; FA58c_2; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW ATP-binding; Glycoprotein; phosphorylation; Receptor; Transferrase;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 840
SQ SEQUENCE 840 AA; 94950 MW; 5D95656C5F53801A CRC64;

Query Match 48.4%; Score 2387; DB 11; Length 840;
Best Local Similarity 52.0%; Pred. No. 13e-181;
Matches 478; Conservative 115; Mismatches 221; Indels 106; Gaps 16;

QY 10 LILLVLVSGDAMKQAFDPKACRYALGMODRTIPDSISASSSSSDSTAARHLSSESDG 69
Db 6 LILLVLVSGA--KAQVNPALCRYPPLGMSGHIDEDITASSQSESTAAKYGRDSEEG 63
QY 70 DGAMCPAGSVPEKEEYLOVDLQRLHLVALVGTGRRHAGLGKEFSRSYRLRYSRGR 128
Db 64 DGAMCPRIQPPDDKLFQDLDTLTLFLLVGTGRRHAGLGKEFYAPMKINYSRSGTR 123
QY 129 MWGKDRMGQEVISGNEDEPGVYLKDLGPPVYARLVRFYPRADRYMSYCLRVLYGCLWR 188
Db 124 WISWRNRHKGQVLDGNSNPYDFLKLDEPPIVAREVRLIPTVDSHSMVCKRVELYGCWVL 183
QY 189 DGLLSTYAPVQGMVYL--SEAVYINDSTYDGHVVGGLQYGGGLADGVVGLDDFRKSOE 246
Db 184 DGLVSTYAPAGQGVFLPGGSIYINDSVYDG--AVGYSMTGGLQYGGGLADGVVGLDDFTOTHE 242

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OY 247 LRVMPGIDYVGMNSHSFSSGYSVEEMEFEDRLRAFOAMQVCHNNMHTLGARLPGVECFR 306
 DB 243 YHWMPGIDYVGMNSHSFSSGYSVEEMEFEDRLRAFOAMQVCHNNMHTLGARLPGVECFR 301
 OY 307 RGVAMAMEGEPHMLNGLNDRPARAVSYLGRVAFLOCFRLFAFWLFLSELSFIS 366
 DB 302 RSEASEMEPTAVSFPLVDVNSARFVYPLQDRMASAKCYHFDATMMSEITFOS 361
 OY 367 D-VVNNSSPALOGTPPPAPMPPGPPPTNFSLELEPPGQOVAKAEGSPYAILIGLV 424
 DB 362 DAAMNNS-----GALPTSP-----MAPTYDMLKYDSDNTIRLLIGLV 401
 OY 425 AIIILLLIITALLMLRMLHRRLSKAERYLEELVHLSVPGDTILINR-----PGRE 480
 DB 402 AIIIFILLIIVIIIMROFQOKMLFKASRRLDDEMTVSLSPSSSMFNSSSPSEOE 461
 OY 481 P-----PPYOEPPRGNPNPSAPCVNGSALLSNPAYRLLATYARPPGPGP 529
 DB 462 SNSTYHRIPLRPDYOE-----SRLIKRLEP----- 489
 OY 530 PTPAMAKPTNTQAYSGDYMEPEKPGAPLPPPPQNSVPHYAEADIVTLQGVGTGAYP 589
 DB 490 -----APGEESGSSGVKPPAPNGP-----EGVPHYAADIYNLQGVGTGNTYSP 536
 OY 590 ALPPGAVGDPPIRY-DFPRSRLRFEKELGEGOGEVHLCEDVSDPOLVSLDPLNTRKH 648
 DB 537 ATMTLLSKRDVAEEFPFKLLTFKKMGEGEVHLCEDVSDPOLVSLDPLNTRKH 596
 OY 649 PLLVAVKILRPDATKNAFSLFRNDLFEVKYIMSRKDPNIIIRLGLVCQODPLCMIT 708
 DB 597 PLLVAVKILRADANKNA-----RNDLFEKIMSRKDPNIIIRLGLVCITDDPLCMITE 650
 OY 709 YVENDLNQFLSAHOLEDKAAGAPEDGQAAGPITSYMLLHVAQAISGMRYLATLNF 768
 DB 651 YVENDLNQFLSRHPLSLSSCSNA-----TVSYNVLKFMATQIASGMKYSLSNF 700
 OY 769 VHRDLATRNCLVGENPTIRIADFGMSRNLXAGDYRVQGRVAVLPIPMMAECLIMKFTT 828
 DB 701 VHRDLATRNCLVGENPTIRIADFGMSRNLXAGDYRVQGRVAVLPIPMMAECLIMKFTT 760
 OY 829 ASDVAVFVTLMEVLMCLCAQPPFCOLTDEQVLENGAEFPFDGQGVYLSRPPACPGLYE 888
 DB 761 AGDVAVFVTLMEVTLMEVTLMEVTLMEVTLMEVTLMEVTLMEVTLMEVTLMEVTLME 820
 OY 889 LMLCRWSRSEORPPFSOLH 908
 DB 821 LMLSCMRRETKHRPSFOETH 840
 RESULT 3
 064108 PRELIMINARY; PRT; 220 AA.
 AC 064108;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE REEFPOR TYROSINE KINASE (FRAGMENT).
 GN PTK-31.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95320273; PubMed=7597135;
 RA Sakuma S., Sawa H., Iijichi A., Toffion P.J.;
 RT "Radiation induction of the receptor tyrosine kinase gene Ptk-3 in
 RT normal rat astrocytes";
 RT Radiat. Res. 143:1-7(1995).
 DR EMBL: S77585; AAB34728.1; -.
 KW kinase.
 FT NON_TER
 SQ SEQUENCE 220 AA; 23670 MW; B9A08E5E3E43F61B CRC64;

Query Match 23.5%; Score 1159; DB 11; Length 220;
 Best Local Similarity 98.6%; Pred. No. 1,7e-84;
 Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 404 GQOPVAKAEGSPYAILIGLVAILLLIILALMLRMLHRRLSKAERYLEELVH 463
 DB 1 GQOPVAKAEGSPYAILIGLVAILLLIILALMLRMLHRRLSKAERYLEELVH 60
 OY 464 SVPGDTILINRPPGPPPPYOEPPRGNPNPSAPCVNGSALLSNPAYRLLATYAR 523
 DB 61 SVPGDTILINRPPGPPPPYOEPPRGNPNPSAPCVNGSALLSNPAYRLLATYAR 120
 OY 524 PRGPGPTPAMAKPTNTQAYSGDYMEPEKPGAPLPPPPQNSVPHYAEADIVTLQGV 583
 DB 121 PRGPGPTPAMAKPTNTQAYSGDYMEPEKPGAPLPPPPQNSVPHYAEADIVTLQGV 180
 OY 584 NTYAVPALPPGAVGDPPIRYDFPRSRLRFEKELGEGOGFE 623
 DB 181 NTYAVPALPPGAVGDPPIRYDFPRSRLRFEKELGEGOGFE 220
 RESULT 4
 0952V7 PRELIMINARY; PRT; 797 AA.
 AC 0952V7;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN F11D5.3A.
 GN F11D5.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None.
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium";
 RT Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA "Nhan M.;
 RT "The sequence of C. elegans cosmid F11D5.3";
 RT Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission";
 RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U41532; AAK68319.1; -.
 SQ SEQUENCE 797 AA; 90302 MW; C96D16AFEL44899E CRC64;
 Query Match 21.2%; Score 1044; DB 5; Length 797;
 Best Local Similarity 29.2%; Pred. No. 1.6e-74;
 Matches 273; Conservative 155; Mismatches 323; Indels 184; Gaps 31;
 OY 9 LILLLVASGDDMGHDPKACRALGMQRTIPDSISASSMS-DSTARHSRLSS 67
 DB 3 LLLYLVGVFHSNTVALELRECSHQIGMSNRKIRDEISASSSPDLQSTPOHARHQE 62
 OY 68 DGDGAMCPAGSVFPKEEYLVLDLRLHLVAVLVTGQGHAGAGLGEFESRYRLRSRDC- 126
 DB 63 SSGSAMCPKQKQINSLSKEMLOLSFSVDVYITSVEQGFDDGRGHEVATARKIQWPSL 122
 OY 127 RRMGMKDRMGOEIVSGNDEGVVLLKDLGPPMAVRLVFPYPRADRVNSVCLRVELYGCL 186

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Db 123 NAAASYKDFELETIPANNDEHAIRRHRLAIRIRIATVPANSYRTVCMREVEGCP 182
QY 187 WRDGLLSTAVAGQTMVLTSEAVYINDSTYGHVYGGIQT -GGGLQADGVYGGDLPFKSQ 245
Db 183 FDDSLVFNVDQGG--LQSGISTYHDSYDGNLANSPLHTGIGKLDGEGKNNFVNH 239
QY 246 ELRWVPGDYVGMGNHSSFGSYVEFEFDRLRAFOAMOVHNNMHTLGARLPGVCECRF 305
Db 240 -----HKWVGMRK--RNGNVKLAPEFSELRNISILHTSN-----EF 276
QY 306 RRGPMAMEEPMRNLG-----NLGDP-----AAVSVPLGGRVARELQCRFL 351
Db 277 KKS-AKAFSSATVLFSGNGKDSPTIVHFNPNDETESEVPRMIRIPVNNRIAKAKIRLN 335
QY 352 FA--GFWLLESEISFIDVYN---ASSPALGCTFPAPMPPPPPTNSSLELEFRGQ 405
Db 336 FGTDSDMLFISEVNFESNHNIELLNDVYI-----PDSVSYSFVTEHDDGT 382
QY 406 QPVAKAGSPFALIGCTVAIIILLILILMLRLHMRRLS-----KAERVLEBELT 460
Db 383 -----SMFAPII--FFMFELIVAVIILVLYRKREYKAKSSPSPNAKREIL----- 427
QY 461 VHLSPGDTLLNNRPPRPPYQEPDRPPGNPHSAPCVNGSALLLSNPAYRLLATY 520
Db 428 --LTIDGNTIKHH-----VSPSTYQMAR-----DNLQNALIEKMPSPITSDY 468
QY 521 ARPRGCGPTLPAMAKPTNT---QAVSGDYMEPEKPGAPLPPPPONSVHYAEADIVTL 577
Db 469 AEPDISVCSDVTA-----NTPPLLYGIDPY-DTQKRSNP-----SSMVKYSDY----- 511
QY 578 QGVGTGNTYAVPALPPGAVDGGPRVDFPRSRLEFKELGEGPGEGVHLCEVSPDOLVS 637
Db 512 -----GEVYCT-TLP-----EIAADKLICVSRIOGEGEVLDQLEN----- 548
QY 638 LDPELVNRKQHPLIVAVKILRPDANKASFLPSRNDLEKVKIMSKDPNIIIRLLGVC 697
Db 549 -----RK-----VAVKKLH-----GISQADEFSFHREIRVIGSLKHPNVEVYVC 589
QY 698 VODPCLMINDYMGNDLGNFLSAHQLEDKAEBAPDGOAOGPTISYMLLHVAAQIA 757
Db 590 TIOKPIICIMEYENGSLKSYI-----LNKPTIQTQSCISICTOLA 630
QY 758 SGMYIATLNFVHRDLATRNCLVGENFTIKIADFGMSRNLVAGDYVVOGRAVLPFRMA 817
Db 631 AGIAYLESCHFVRHDIAARNCIYDGBGNVAKIADFGMARSLXSOEYIVVEKQVLPFRMA 690
QY 818 WECLMGKFTTASDVNAFVTLMEVLMLCRAOPPGQITDQVIEAGFEFRDQGRQYLLS 877
Db 691 WEALLLCKFSTASDVNMGFGVTMEIFSLCESEKPYSDMTDDVVENLQSMSTGSLKQVLS 750
QY 878 RPPACPGGLY-ELMLRCMSRESQORPPFSQLHREL 911
Db 751 RPPACPSKLIYNEQILPCWNTESSRPFSENVHLHL 785

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RESULT 5
0952V6 PRELIMINARY; PRT; 767 AA.

AC 0952V6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE HYPOHETICAL PROTEIN F11D5.3B.
GN F11D5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;

RA None;
RT "genome sequence of the nematode C. elegans: a platform for
RT Investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Nham M.;
RT "The sequence of C. elegans cosmid F11D5.";
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41532; AKG68320.1;
SQ SEQUENCE 767 AA; 86900 MW; 2953C06B9416F2EE CRC64;

Query Match 20.8%; Score 1023; DB 5; Length 767;
Best Local Similarity 29.3%; Pred. No. 7,4e-73;
Matches 266; Conservative 149; Mismatches 308; Indels 184; Gaps 31;

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QY 37 MODRTIPSDISASSMS-DSTARHSRLSSDDGAMCPAGSVFPEEETLVQVLDQLH 95
Db 1 MSNRKIDEDQISASSSFDLQSTGPHARAOESGAMCRNQINSKELQISFSDVT 60
QY 96 LVALVGTQGRHAGLGKFSRSYRLARYSRDG-RRMGMKRMGQEVISGNEDEPGVYLKD 154
Db 61 VITSVETQGRFDORGMEYATAFRIQYWRPSLNMASGYKDFELETIPANNDEHAIRRH 120
QY 155 LGPRMVARLRFYPRADRVMSVCLRVLLGCLMRDGLLSTAPVQGMVYSEAYINDST 214
Db 121 LDRRIARRIRIVPVSSTFYVCMREVEFGCPDSDSLVFVNDQGD--LQSGISTYHDS 177
QY 215 YDGHVVGLOY -GGGLQADGVYGGDLPFRKSOELRWVPGDYVGMGNHSSFGYVMEFE 273
Db 178 YDGLNLSPLHTGIGKLDGEGVKNVFNH-----HKWVGMRK--RNGNVKLAPE 228
QY 274 FDLRAFOAMOVHNNMHTLGARLPGVECRFRRGPMAMEGEMRNLG-----N 325
Db 229 FSELNRISGILHTSN-----EFKKS-AKAFSSATVLFSGNGKDSPTIVH 273
QY 326 LGDPR-----AAVSVPLGGRVARELQCRFLA -GFWLLESEISFIDVYN---NSS 373
Db 274 FNNPDETESEVPRMIRIPVNNRIAKAKIRLNFQTDSDMLFISEVNFESNHNIELLND 333
QY 374 PALGTFPPAPMPPGPPPNFSSLELEPRGQGVAKAESPTAILIGCTVAIIILLILI 433
Db 334 VVI-----PDSVSYSFVTEHDDGT-----SMFAPII--FFMFELIVAVI 370
QY 434 IALMLRLHMRRLS-----KAERVLEBELVHLVSPGDTLLNNRPPRPPYQEP 488
Db 371 ILTVLYRKREYKAKSSPSPNAKREIL-----LTIDGNTIKHH-----VSPSTYQMAR 418
QY 489 PRGNPPHSAPCVNGSALLLSNPAYRLLATYARPPGCGPTLPAMAKPTNT---QAVSG 545
Db 419 -----DNLQNALIEKMPSPITSDYAEPPDISVCSDVTA-----NTPPLLYGIDG 461
QY 546 DYMEPEKPGAPLPPPPONSVPHYAEADIVTLQVGTGNTYAVPALPPGAVDGGPRVDF 605
Db 462 FY-DTQKRSNP-----SSMVKYSDY-----GEVYCT-TLP-----EI 492
QY 606 PRSRLFRKELGEGVHLCEVSPDOLVSLDFPLNVRKQHPLIVAVKILRPDATKNA 665
Db 493 ARDKLICVSRIOGEGEVLDQLEN-----RK-----VAVKKLH----- 527
QY 666 SFLEFRNDLEKVKIMSKDPNIIIRLLGVCVQDDPCLMINDYMGNDLGNFLSAHQLE 725
Db 528 GISQADEFSFHREIRVIGSLKHPNVEVYVGTIOKPIICIMEYENGSLKSYI----- 581
QY 726 DKAAGCAPDGOAOGPTISYMLLHVAAQIASGMRYLATLNFVHRDLATRNCLVGENFT 785

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Db 582 -----LKNPTIOTSICITQGLAAGLAVLSCNFVHDIARNLTVDEGN 628
OY 766 IRIADPGSRNIYAGDYRVQGRVAVPIRMAMAECLIMKFTTASDVMAFGVTLMEVLM 845
Db 639 VRIADPGSRNIYAGDYRVQGRVAVPIRMAMAECLIMKFTTASDVMAFGVTLMEVLM 845
OY 846 CKAOPFGOLTDEOVYENGEFFRDGROYVLSRPACPGGLY-ELMLRCMSRSEORPPF 904
Db 669 CSEKYSMDTDDVYENLQSMSTGSLKOVLSRPRMPSKLSLNEOITPCWNYESSRPSF 748
OY 905 SOLHREFL 911
Db 749 ENVHHL 755

RESULT 6
ID 064107 PRELIMINARY: PRT: 183 AA.
AC 064107:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE RECEPTOR TYROSINE KINASE (FRAGMENT).
GN PK-35.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95320273; PubMed=7597135;
RA Sakuma S., Saza H., Tjichi A., Tofillon P.J.;
RT "Radiation induction of the receptor tyrosine kinase gene pk-3 in
RT normal rat astrocytes."
RL Radiat. Res. 143:1-7(1995).
DR EMBL: S77556; AAB34729.1;
KW Kinase.
FT NON_TER
SQ SEQUENCE 183 AA; 19717 MW; 66DE2709B5E4A832 CRC64;

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Query Match 18.9%; Score 929.5; DB 11; Length 183;
Best Local Similarity 81.8%; Pred. No. 2.6e-66;
Matches 180; Conservative 0; Mismatches 3; Indels 37; Gaps 1;

OY 404 GQOPVAKAEGSPITALICGLVAIIILLLIITLMLRLHMRLLSKAERRVLEELTVHL 463
Db 1 GQOPVAKAEGSPITALICGLVAIIILLLIITLMLRLHMRLLSKAERRVLEELTVHL 60
OY 464 SVPGDTIILNRPGRPREPPYQEPFRGNPPHSAPCVNGSALLISNPAYRLLATYARP 523
Db 61 SVPGDTIILNRPGRPREPPYQEPFRGNPPHSAPCVNGSALLISNPAYRLLATYARP 103
OY 524 PRGCGPTPAMAKPTNMGVSGDYWEKPGAPLPPPPNSVPHYAEDIVTGGVGG 583
Db 104 -----SGDIMEKPGAPLPPPPNSVPHYAEDIVTGGVGG 143
OY 584 NTYAVPALPPGAVDGPVRVDFPRSRLLRKKELGSGFGE 623
Db 144 NTYAVPALPPGAVDGPVRVDFPRSRLLRKKELGSGFGE 183

RESULT 7
ID 018433 PRELIMINARY: PRT: 700 AA.
AC 018433:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE RECEPTOR TYROSINE KINASE.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;

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OC Astrophorida; Geoditidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224609; PubMed=9060390;
RA Gamulin V., Skorochood A., Mueller M., Schaecke H., Mueller W.E.G.;
RT "Experimental indication in favor of the introns-late theory: The
RT receptor tyrosine kinase gene from the sponge Geodia cydonium."
RL J. Mol. Evol. 44:242-252(1997).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: X94128; CA63848.1;
DR HSSP: P08631; IAD5.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR020111; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00069; pkinase_1.
DR SMART: SM00409; IG_1.
DR SMART: SM00410; IG_Like; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 700 AA; 77851 MW; 74953FC82D820B6C CRC64;

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Query Match 14.0%; Score 691; DB 5; Length 700;
Best Local Similarity 32.2%; Pred. No. 2e-46;
Matches 193; Conservative 87; Mismatches 193; Indels 126; Gaps 20;

OY 409 AKAEGSPITALICGLVAIIILLLIITLMLRLHMR-----MLRLHMR----- 445
Db 136 SNSGSGNSGVINGVLTLLIITLIIILFVWVYCYRRGRGFDLGSCELSGSCGCV 195
OY 446 ILSKAERVLEELTVHLSVPGDTIILNRPGRPRE-----PYQEPFRGN--PPHSAP 498
Db 196 ILSKAERVLEELTVHLSVPGDTIILNRPGRPRE-----PYQEPFRGN--PPHSAP 255
OY 499 CVPNGSALLISNPAYRLLATYARPGRGPTPAMAKPTNQAASGVMEPEKGAFL 558
Db 256 -----LTTTELNEMLSIDKEELSPFOEKP--RRNTGLSTYSQSGTTPKLAKTKL 307
OY 559 PPPNSVPHYAEDIVTLQ-GVTGNT-YAVPALP----- 592
Db 308 RFFKKNRPNIYQSVLVLELELDVNTLYALPLPNSTRNSASTDDLASPIYVAIN 367
OY 593 -----FGAVD-----GP-----PRVDFPRSRLLRKKELGSGFGEVHL 627
Db 368 PSMFTKRSTSTGNDDLPHPGPIYARPIQOKMRPLSVNIRRYKQIGVGFVAVIA 427
OY 628 EYD--SPDVLSDPPLNVRKGH-----PLVAVYILRPDADTKNASFSLSNDLKEVK 680
Db 428 EYDGLSGSNVSLP-----KSNMADGVALYAVKLLPVDSDV-----RQSDKEIK 475
OY 681 ILSRLKDPNIIRLLGVQVODDPLCMITIDYMEGNDLQELSAHOLEDKAAEGAPGDGAQ 740
Db 476 FMSQLQHDHSIVQLAVCHSKHPFYMEYMEGNDLQELQKQVMD-----DSDSLY 527
OY 741 GETIYPMILHRAQIYAGMRYLATLNVYHDLATRNCLVGENFTIKTADGSRNLYAG 800
Db 528 SNQIPSTLLVYAVQIYAGMYLSSLNLYHDLATRNCLVSNFRKIKSDGSRNLYER 587
OY 801 DYRYQGRVAVPIRMAMAECLIMKFTTASDVMAFGVTLMEVLMCKRAOPFGOLTDEOVI 860
Db 588 VYRYRGRVAVPIRMAMAECLIMKFTTASDVMAFGVTLMEVLMCKRAOPFGOLTDEOVI 646

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QY 861 ENAEFFRDGROYLLSRPPACPOGLYELMRCMSRSEORPPPSQLHRELAEDALNTV 919
DB 647 QDA---INGTGRR-MGRPECCPOAVYEVLLRCWEYAAADRAFTEKH-----DSLMLI 696

RESULT 8
ID 09BKL8 PRELIMINARY; PRT; 1145 AA.
AC 09BKL8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ROR.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
OC Aplysiidae; Aplysia.
OC NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RA McKay S.E., Hislop J., Scott D., Bulloch A.G., Kaczmarek L.K.,
RA Carew T.J., Sossin W.S.;
RA "Aplysia for, a member of the Trk/Musk family of receptor tyrosine
RT kinases, forms clusters on the surface of identified neuroendocrine
RT cells.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AF216782; LAK25726.1; -.
DR HSSP: P11362; 1FGK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR003598; Ig.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_1like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00409; Ig_1.
DR SMART: SM00408; Ig_c2; 1.
DR SMART: SM00410; Ig_1like; 1.
DR SMART: SM00130; KR; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyRKc; 1.
DR PROSITE: PS50038; Fz; 1.
DR PROSITE: PS50021; UNKNOWN_1.
DR PROSITE: PS50070; KRINGLE_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
DR ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;
KW Receptor; Transferase; Transmembrane.
SQ SEQUENCE 1145 AA; 123622 MW; 5C49FA6E2A9D1ABD CRC64;

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Query Match 13.1%; Score 648; DB 5; Length 1145;
Best local similarity 31.8%; Pred. No. 1, le-42;
Matches 187; Conservative 74; Mismatches 149; Indels 178; Gaps 24;

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QY 445 RLISKARVLEEL--YVHL-----SVPDITLIN-----NRGPRE-----PPPY 484
DB 310 RKICRDEALENDICRTETILAKRHNLIGDNLPCSQLCGTGREGDNCIRIGMPGS 369
QY 485 QERPR---GNPHSAPCPVNSALLSNPAYULLATATAPRR---GGPPPPAAK-- 536
DB 370 TSGRGHPKGGNPSWNP-----GTRDPGRSGSGSKRPTSDKDT 410

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QY 537 -----PTNQAVSG-----DYMEPE-----KPGAP 556
DB 411 GRGGGPTDYCYTGRGNTNGEYVSXSGFMCLGMKMDSGFELGDHNYCANPNRREAP 470
QY 557 LL-----PPPNVSP-----HYEADIVTLQVGTGNT---YAVPALP-PGAVG- 597
DB 471 WCFTRDKRMPKELCAVPCSDYDEGHSEAD-----EGSNKLMYILIPSLTVPLALGI 523
QY 598 -----DGPFRDPRSRRLREKXIGEFG 622
DB 524 LLALICQCSNHTRASRPNNKQAPVEMSPLNPKSASRAPEFPMNRLFQELGEGAFG 583
QY 623 EVHLCEVDSPODVLSDPLNVRKGHPLVAVKILRPDATTNASEFSLFRNDLFKEVIM 682
DB 584 KVVYGE-----LVGLGESSV-----TTVAIKTLKENALKV-----QNDPREVDLM 626
QY 683 SRLKDPNIIIRLLGVCVODDPLCMITDYMENDLNOFLSAN--QEDKAAGAPDGOAAQ 740
DB 627 SDMRHPNIVCLLGVCMKQEPWCMLEFYMAQGDLEHLLSHSPHSDVYVAEDDSGTG--G 683
QY 741 GPRTSYMLHVAQIASGMRKYLATLNFVHRDLATRNCLVGEENTTIKADGMSRLYAG 800
DB 684 GHILEYSEMLHVSQVAAAGMYLASHHFRVHDLAARNILVADGLTVKISDGLSRDVS 743
QY 801 DYRVQGRAVLPFRMAMECTIMGKFTTASDVMAFGVTLFVLMLCRAOPGOLDEQVI 860
DB 744 DYIVQSKSLPLPYRMPEALILYKFTTSDVMAFGVYLVMEVSY-GLOPTYGSSNOEVI 802
QY 861 ENAEFFRDGROYLLSRPPACPOGLYELMRCMSRSEORPPPSQLH 908
DB 803 EMI-----RSRI-LGCPCECPARIYIGLVMECHHMPARRPPREH 843

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RESULT 9
ID 09YH43 PRELIMINARY; PRT; 811 AA.
AC 09YH43;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE NEUROTROPHIN RECEPTOR B XTRKB-ALPHA.
GN XTRKB.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodidae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Islam N., Gagnon F., Moss T.;
RA Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb
RT mRNA are expressed in a pseudo-segmental manner within the early
RT xenopus central nervous system.*;
RL Int. J. Dev. Biol. 40:973-983(1996).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: U39671; AAD00002.1; -.
DR HSSP: P06213; 1IRK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00560; LRR; 1.
DR Pfam: PF01463; LRCT; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00409; Ig; 1.

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DR SMART; SM00082; LRRT; 1.
 DR SMART; SM00013; LRRT; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;
 KM Transmembrane; Tyrosine-protein kinase
 SO SEQUENCE 811 AA; 91249 MW; C67CDICF132C1CF5 CRC64;

Query Match 12.8%; Score 633; DB 13; Length 811;
 Best Local Similarity 44.7%; Pred. No. 1e-41;
 Matches 139; Conservative 48; Mismatches 80; Indels 44; Gaps 9;

QY 607 RSLRFRKELGEGQFGEVHLC---VDSPODLSLDFPLNVRKGPPLVAVKILRPDATK 663
 DB 524 RHNIVLKRLEEGAGFKVFLAECYNLYPED-----KILVAVKTLK-DASD 568
 QY 664 NASFSLSRNDPLKEVKIMRLDPIIRLLGCVQDDPLCMITDYMNGDLNQLSAHQ 723
 DB 569 NA-----RDFRREELLTNLQHEHLYKFGVCEGDPIMVEYMKHGDINKFLRAH- 621
 QY 724 LEDKAAGAPGDGAAG---PTISYPMILHVAQAISGMYLATLNFVHRDLATRNCLV 780
 DB 622 -----GPDVAVLAEGRNPAELTOSQMLHIAQIAAGVYLLASQFVHRDLATRNCLV 673
 QY 781 GENFTIKIADFGMSRLYAGDYRYVOGRAVLPIRMAMECILMGKFTTASDVAFGYTLW 840
 DB 674 GEMLVKIGFGMSRDYSDYRYVGHTMLPIRMMPESIMYKFTTESVMSLGYVLW 733
 QY 841 EVLMICRAQPFQGLTDOVIEENAGEFFRDGROYLISRPACPGGLYELMRCRSRESEQ 900
 DB 734 EIFTYGR-QPWYQLSNNEVICT-----TOGR--VLORPRCPREYVDLMGCMQRPBM 785
 QY 901 RPPFSQLRFL 911
 DB 786 RLNIKEIHSIL 796

RESULT 10
 Q9YH44 PRELIMINARY; PRT; 821 AA.
 AC Q9YH44: 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE NEUROTROPHIN RECEPTOR B XTRKB-ALPHA.
 GN XTRKB.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97101727; PubMed-8946245;
 RA Islam N., Gagnon F., Moss T.;
 RT Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb
 RT mRNA are expressed in a pseudo-segmental manner within the early
 RT Xenopus central nervous system.";
 RL Int. J. Dev. Biol. 40:973-983(1996).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL; U39670; AA000001.1; -
 DR HSSP; P06213; IIRK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003599; 19.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000372; LRR_Nterm.

DR InterPro; IPR002011; Receptor_tyr_kin_II.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00560; LRR; 1.
 DR Pfam; PF01463; LRRT; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00082; LRRT; 1.
 DR SMART; SM00013; LRRT; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;
 KM Transmembrane; Tyrosine-protein kinase
 SO SEQUENCE 821 AA; 92311 MW; 0AF81BE74F08FED3 CRC64;

Query Match 12.8%; Score 633; DB 13; Length 821;
 Best Local Similarity 44.7%; Pred. No. 1e-41;
 Matches 139; Conservative 48; Mismatches 80; Indels 44; Gaps 9;

QY 607 RSLRFRKELGEGQFGEVHLC---VDSPODLSLDFPLNVRKGPPLVAVKILRPDATK 663
 DB 534 RHNIVLKRLEEGAGFKVFLAECYNLYPED-----KILVAVKTLK-DASD 578
 QY 664 NASFSLSRNDPLKEVKIMRLDPIIRLLGCVQDDPLCMITDYMNGDLNQLSAHQ 723
 DB 579 NA-----RDFRREELLTNLQHEHLYKFGVCEGDPIMVEYMKHGDINKFLRAH- 631
 QY 724 LEDKAAGAPGDGAAG---PTISYPMILHVAQAISGMYLATLNFVHRDLATRNCLV 780
 DB 632 -----GPDVAVLAEGRNPAELTOSQMLHIAQIAAGVYLLASQFVHRDLATRNCLV 683
 QY 781 GENFTIKIADFGMSRLYAGDYRYVOGRAVLPIRMAMECILMGKFTTASDVAFGYTLW 840
 DB 684 GEMLVKIGFGMSRDYSDYRYVGHTMLPIRMMPESIMYKFTTESVMSLGYVLW 743
 QY 841 EVLMICRAQPFQGLTDOVIEENAGEFFRDGROYLISRPACPGGLYELMRCRSRESEQ 900
 DB 744 EIFTYGR-QPWYQLSNNEVICT-----TOGR--VLORPRCPREYVDLMGCMQRPBM 795
 QY 901 RPPFSQLRFL 911
 DB 796 RLNIKEIHSIL 806

RESULT 11
 Q9PST9 PRELIMINARY; PRT; 486 AA.
 AC Q9PST9: 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE NEUROTROPHIN RECEPTOR B XTRKB-BETA (FRAGMENT).
 GN XTRKB.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97101727; PubMed-8946245;
 RA Islam N., Gagnon F., Moss T.;
 RT Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb
 RT mRNA are expressed in a pseudo-segmental manner within the early
 RT Xenopus central nervous system.";
 RL Int. J. Dev. Biol. 40:973-983(1996).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

DR EMBL: U39672; AAD09444.1; --
DR HSSP: P06213; LRR.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; tyr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00219; TyrcK.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II.1.
DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;
KW Transmembrane; Tyrosine-protein kinase.
FT NON_TER
SQ SEQUENCE 486 AA; 54546 MW; 1645869ABE78274F0 CRC64;

Query Match 12.8%; Score 631; DB 13; Length 486;
Best Local Similarity 44.1%; Pred. No. 7.1e-42;
Matches 137; Conservative 50; Mismatches 80; Indels 44; Gaps 9;

QY 607 RSRLNFKKLEGGFGEVHLCEVDS---PDLVSLDFPLNVRKQHPILVAVKILRPDQTK 663
DB 199 RHNIVLKELEGAGFAGKVFLECYNLYLEQD-----KIIVAKTLK-DASD 243
QY 664 NASLSLFRNDFLEKVKMSRKADPNIRLLGVCVQDDPLCMITDYMENGDLNQLSAHQ 723
DB 244 NA-----RKDFHREALLTNLOHENTYKFGVCVEGDPILNVEFVKGHGLNFKFLRAH- 296
QY 724 LEDKAAEGAPGDGAAGS---PTISYPLMLHVAAGIASGMVLYATLNVVHDLATRNCLV 780
DB 297 -----GPAVLMAEBENLAEFTOSQMLHISQILAGMYLLASQHHVDLATRNCLV 348
QY 781 GENFTIKIADFGSMRLVAGDYRVQGRAVLPIRMAMECILMKETFTASDVMAFGVYLM 840
DB 349 GENLIVKIGDGMGRDYSTDYRVGHTMLPIRMMPESIMYRFTESVMSGLVYLM 408
QY 841 EVMILCRAGPFGQLTDEVIYNAEFPDQGRQVLYSRPACPGGLYELMIRCSRESEQ 900
DB 409 EITFYGK-QPMYQLSNNEVICI-----TQGR-VLQRPRTCPKEIYDLMIGMCQREPHM 460
QY 901 RPPFSQHLRFL 911
DB 461 RLNIKEIHSLL 471

RESULT 12
Q090699 PRELIMINARY; PRT; 790 AA.
AC Q090699;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, last annotation update)
DE TROPOMYOSIN RECEPTOR KINASE.
GN CYRKA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Schrempel A., v Schack D., Dechant G., Barde Y.A.;
RT "Early expression of the nerve growth factor c-tyrA in chicken
RT sympathetic and sensory ganglia.";
RL Mol. Cell. Neurosci. 6:0-0(0).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: U43396; AAA83289.1; --
DR HSSP: P11362; IFGR.
DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR003599; IG.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; tyr_pkinase.
DR Pfam: PF00047; IG.1.
DR Pfam: PF00560; LRR.2.
DR Pfam: PF01463; LRCT.1.
DR Pfam: PF00069; pkinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00409; IG.1.
DR SMART: SM0082; LRCT.1.
DR SMART: SM00219; TyrcK.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II.1.
DR ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 790 AA; 88669 MW; AD2314608F30AD71 CRC64;

Query Match 12.8%; Score 628.5; DB 13; Length 790;
Best Local Similarity 30.6%; Pred. No. 2.3e-41;
Matches 193; Conservative 78; Mismatches 188; Indels 171; Gaps 23;

QY 356 MLTSEISFIDVYNNSSPALGTFPPAPMPPGPPPNFSSLELPDQGVAKAESSP 415
DB 237 WEVLLEINNISSSLNHK-----DLTCAENAVGLAEDS- 269
QY 416 TAILIGCLVALILLILLIALLMLRHLNR-----RLLSKAERVRLEETVHLVS- 465
DB 270 -VMLNVEFPYVILLLESLIPQHFNCIPESVDSNPTRILMLFNSGMLPEGYIHRIYEX 328
QY 466 -PGOTILIN---NRQPREPPYQEPFRGNPPHSACVNGS-ALLSNP---AYRL 516
DB 329 EPNSTVHLGCLQILNR-----PH---VNNGVYTLVQNPDLGRATRSI 367
QY 517 LATYARPP--RGPPPTPAMAKPTNTQAYSGDYMEPEKCAPLPPPPNSVPHYAEDI 574
DB 368 QGRFMDNPFSEPEEPIPVISPLGTRNS-----LEGPEVTADETFGVSV 414
QY 575 VTIGV-----TGNTYAVPA-----LPPGAVGDP 600
DB 415 AVALAFAFLSVMLIALNKGHRKSGKIRSAVLAQEDOLANSIMFMNCGSSPVSTE 474
QY 601 PRVD-----PPSRRLFKFKLEGGFGEVHLCEVDS--PDLVSL 638
DB 475 SKLDGLKSNFLENPOYFCNACVHHQRRDYLKWELEGAGFVLECSHLPEQ---- 530
QY 639 DFLNVRKQHPILVAVKILRPDQTKNASFSLFSNDELKVKIMSRKDPNIRLLGVCV 698
DB 531 -----EKLVAVALK-EVTESA-----RLDQREAEILLVQHEHIVFYGVCT 574
QY 699 QDDPLCMITDYMENGDLNQLSAHQLEDAEGAPGDGAAGPTISYPLMLHVAAGIAS 758
DB 575 EGEPLIVFEYMKRGDLNRLFRLSHGPDAKIID--QGQGGQCGGLTLH--MLQATQIAS 630
QY 759 GMRYLATLVVHDLATRNCLVGENFTIKIADFGSMRLVAGDYRVQGRAVLPIRMAMP 818
DB 631 GMVYLAHLFVHDLATRNCLVGHDLVYKIGDFMSHDISTDYRVGGRMTLPIRMAPP 690
QY 819 ECLMGKFTASDVMAFGVTLMEVLMICRAGPFGQLTDEVIYNAEFGPFDQGRQVLYSR 878
DB 691 ESTILYKRFTEESDIMSGLVLMELFTYKQ-QPMYQLSNTEAIECT-----TQGR- 742
QY 879 PPAPOGLYELMIRCSRESEQRPFSQHL 908
DB 743 PRTCPSEVYDIMSQWREPOQRORIIDIH 772

RESULT 13

027656 ID 027656 PRELIMINARY: PRT: 699 AA.

AC 027656:

DT 01-NOV-1996 (TREMBLER. 01, Created)

DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLER. 19, Last annotation update)

DE SPONGE RECEPTOR TYROSINE KINASE (EC 2.7.1.112).

GN GCR 2.

OS Geodia cydonium (Sponge)

OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;

OC Astrophorida; Geodiidae; Geodia.

/OX NCBI_TaxID=6047;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95142935; PubMed=7840899;

RA Gamulin V., Rinkewich B., Schaecke H., Kruse M., Mueller I.M., Werner E.G.;

RT "Cell adhesion receptors and nuclear receptors are highly conserved from the lowest metazoa (marine sponges) to vertebrates."

RL Biol. Chem. Hoppe-Seyler 375:583-588(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=95251882; PubMed=7734153;

RA Schaecke H., Rinkewich B., Gamulin V., Mueller I.M., Mueller W.E.G.;

RT "Immunoglobulin-like domain is present in the extracellular part of the receptor tyrosine kinase from the marine sponge Geodia cydonium."

RL J. Mol. Recognit. 7:273-276(1994).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=97224609; PubMed=9060390;

RA Gamulin V., Skorkhod A., Mueller M., Schaecke H., Mueller W.E.G.;

RT "Experimental indication in favor of the introns-late theory: the receptor tyrosine kinase gene from the sponge Geodia cydonium."

RL J. Mol. Evol. 44:242-252(1997).

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

CC EMBL: X77528; CAA54663.1; -.

DR HSP: P08631; IAD5.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR003599; IG.

DR InterPro: IPR003600; IG_1ike.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR002011; Receptor_tyr_kin_II.

DR InterPro: IPR001245; Tyr_pkinase.

DR Pfam: PF00047; IG_1.

DR Pfam: PF00069; Pkinase_1.

DR SMART: SM00409; IG_1ike; 1.

DR SMART: SM00410; IG_1ike; 1.

DR SMART: SM00219; TykC; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.

KW Arg-binding; Glycoprotein; Kinase; Phosphorylation; Receptor; Transmembrane; Tyrosine-protein kinase.

SO SEQUENCE 699 AA; 77477 MW; 80A8B25AB0851CCE CRC64.

Query Match 12.7%; Score 623.5; DB 5; Length 699;

Best local similarity 31.6%; Pred. No. 4.8e-41;

Matches 195; Conservative 83; Mismatches 176; Indels 163; Gaps 26;

QY 409 AKAGSPALLIGGLVALILLILLIAL--MLRLMRLLSKARRVLEELTVHLS-- 464

DB 136 SNSSGSGNGVAGVILITLILILILIFVWVCYR-----RGKLDGSCRELSCG 189

QY 465 ----VPGDTILNNRGRREPPYQPPRGNGPPHSACVPGSALLLS----- 509

DB 190 SCSCVP-----LLAALKGVKLPTRHRENDK-----NGTLRLRNERNHADTYNE 234

QY 510 --NPAYRLLATYARPPGPGPP-----TPAMKKPT--NT--QAY 543

DB 235 IYSVVKPLKTKISPP--PLPPLLTETELNELTSDKEKELSPIOEKPTRRNTGLSTY 292

QY 544 SCDMEPEKPGAPLLPPPPONSVPNHYAEDIVTLQ-GVTGGNT-YAVPALP----- 592

DB 293 SOSGTFIKLAKTKLRFRKKENPIYQSADELELELDVNDTLVLPSPNSTRNSASF 352

QY 593 -----FGAVD-----GP-----PRVDEPRRLRP 612

DB 353 TDLIASDPIYSVAIINPSMFTKRSSTIGNDLHPGYGIVARPIKOKRKOPLVNSVDNIRE 412

QY 613 KERLGEQGEFVHLCEVD--SPDILSDPLPNVRKSH-----PLVAVKILRPDATKNA 665

DB 413 VKQIGVGFQFVAVVLAETGTSGSNVSLP-----KSNMADGVALYAVKLPDYSDXY 466

QY 666 SEFLFSRNDFLKVKTKMSRLKDPNIIRLLGVCYQDDPLCMITDMNGDNLQPLSAHQLE 725

DB 467 LQ8-----FDKEIKFMSQLQHDHSIVQLLAICHSKHPFIYMEYMNQDNLQGYQW 520

QY 726 DKAAEGAPGGOAAGPPTISYPMILHYAAQIASGMRTLATINVHDLATRNCLVGEINT 785

DB 521 D-----DSDALYSNQIPSTLLYMAVOIASGMYLSSLVYHRLATRNCLVGSNFR 572

QY 786 IKIADFGMSRLYAGDYRYVQGRAVLPIRMAMECITLMGKFTTASDVNAFGVTLMFVLM 845

DB 573 IKISDGMKRLRYRYRYRGRAPLPIRMAYES-FYGFSSKSDAMAGVYWEIYTL 631

QY 846 CRAQPFQGLTDEQVIENAGFEFFDQGOVYLSNP---PACQGLYELMLRCMSRESEORP 902

DB 632 GKQPYEELDDQDMQDA---IRGTGRRI-MGRPRVAGCVRG---AIRCWYAAADRA 683

QY 903 PFSQRLRFLEADLNTV 919

DB 684 TFEIRH----DSLNDI 695

RESULT 14

075682 ID 075682 PRELIMINARY: PRT: 839 AA.

AC 075682:

DT 01-NOV-1998 (TREMBLER. 08, Created)

DT 01-NOV-1998 (TREMBLER. 08, Last sequence update)

DT 01-DEC-2001 (TREMBLER. 19, Last annotation update)

DE TRKC PROTEIN.

GN TRKC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98449483; PubMed=9778053;

RA Ichno N., Rodriguez R., Martin-Zanca D., Gonzalez-Sarmiento R.;

RT "Genomic characterization of the human trkc gene."

RL Oncogene 17:1871-1875(1998).

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

CC EMBL: AJ224521; CAA12029.1; -.

DR EMBL: AJ224522; CAA12029.1; JOINED.

DR EMBL: AJ224523; CAA12029.1; JOINED.

DR EMBL: AJ224524; CAA12029.1; JOINED.

DR EMBL: AJ224525; CAA12029.1; JOINED.

DR EMBL: AJ224526; CAA12029.1; JOINED.

DR EMBL: AJ224527; CAA12029.1; JOINED.

DR EMBL: AJ224528; CAA12029.1; JOINED.

DR EMBL: AJ224529; CAA12029.1; JOINED.

DR EMBL: AJ224530; CAA12029.1; JOINED.

DR EMBL: AJ224531; CAA12029.1; JOINED.

DR EMBL: AJ224532; CAA12029.1; JOINED.

DR EMBL: AJ224533; CAA12029.1; JOINED.

DR EMBL: AJ224534; CAA12029.1; JOINED.

DR EMBL: AJ224535; CAA12029.1; JOINED.

DR HSP: P06213; TRK.

DR InterPro: IPR000719; Euk_pkinase.

DR Interpro; IPR003589; Ig.
 DR Interpro; IPR003006; Ig_MHC.
 DR Interpro; IPR001611; LRR.
 DR Interpro; IPR000483; LRR_Cleav.
 DR Interpro; IPR000372; LRR_Nterm.
 DR Interpro; IPR002011; Receptor_Tyr_Kin_II.
 DR Interpro; IPR001245; Tyr_kinase.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00560; LRRCT; 2.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01462; LRRNT; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR SMART; SM00409; Ig; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00013; LRRNT; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;
 KW Transmembrane; Tyrosine-protein kinase.
 SO SEQUENCE 839 AA; 94428 MW; 7FE846830083C08 CRC64;

Query Match 12.7%; Score 623.5; DB 4; Length 839;
 Best Local Similarity 31.7%; Pred. No. 6.3e-41;
 Matches 174; Conservative 67; Mismatches 131; Indels 177; Gaps 20;

OY 490 RGNPPSACVPRNG-----SALLSNPA-----YRLLATYR 522
 DB 326 RGNPPPTLMLHNGOPRLRSKIIHVEYOGELISEGLFNKPTHYNNNYTLI-----K 381
 OY 523 PRGPPEPTPAMAKPNTQAYSQDYE---PEKGPAPL---PPRPNQSVPTAEADIV 575
 DB 382 NPLG-----TANQTINGHFLKEPPESTDNFLLFDEVSPPTPTVTHKPEEDTF 430
 OY 576 TLQVGTGNTAVPAL-----P 592
 DB 431 GVSINAGLAACVLLVLFVMIKYGSRKFGMKGPVAVISGEEDSASPLHHNHGTT 490
 OY 593 PGAVDGP-----PRVDPP-----NSRLFKKELGEGRG 622
 DB 491 PSLDAGPPTVYIGMTIRIVIEINPOYRQGHNCHEPDTYVOHTRKRDIVLKRKELGEGRG 550
 OY 623 EYHLCVSDPDLVSLDPLNVRKGHPLVAVKILRPDAFKNASFSLSRNDFLKEVKIM 682
 DB 551 KVFLEAC-----YLSPTK-DKMLVAVKALK-DPT-----LAARKDQREAEILL 592
 OY 683 SRLKDPNIRLLGVQVDDPLCMITDMENGDNLNOLSAHOLEDKAAEGAPG-----DQ 737
 DB 593 TNLQEHYIVKFGVCGDGPLIMVFYMKHGDNLKFLRAH-----GPDAMILVDSQ 643
 OY 738 AAGGP-TISYPMILHVAAGIASGRIATLNFVHRDLATRNCLVGENFTIKIADFGMSRN 796
 DB 644 PROAKGELISOMLHIASQIASGMVYLIAQHVFHRLATRNCLVGENFTIKIADFGMSRD 703
 OY 797 LVAGDYR-----VQGRAVLPIRMAMECIIMKFTTASDVMAFGVTLMEV 842
 DB 704 VSTDYIRLFNPSGNDPCWCEYGGHTMLPIRMMPRESIMRKFTTESDVMSFGVTLMEI 763
 OY 843 LMLCRAQPGQLTDEQVLENAGEFFPDGROYLLSRPPACPOGLYELMLRCMSRESEORP 902
 DB 764 FTYGK-QPWFQLSNTEVICI-----TQGR-VLEPRVCPREYVDVLMGCMQREPOQL 815
 OY 903 PFSQHLRL 911
 DB 816 MIKEIKIL 824

RESULT 15
 015655 PRELIMINARY; PRT; 503 AA.

AC Q15655;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 55 KDA PROTEIN.
 GN TRK-TI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92195650; PubMed-1532241;
 RA Greco A., Pierotti M.A., Bongarzone I., Pagliardini S., Lanzl C., Della Porta G.;
 RT "TRK-TI is a novel oncogene formed by the fusion of TPR and TRK genes in human papillary thyroid Carcinomas.";
 RT Oncogene 7:237-242(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92175499; PubMed-1541391;
 RA Hill K., Boone C., Goebel M., Puccia R., Sdicu A.M., Bussey H.;
 RT "Yeast KRE2 Defines a new gene family encoding probable secretory proteins, and is Required for correct N-Glycosylation of proteins.";
 RT Genetics 130:273-283(1992).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL; X62947; CAA4719.1; -.
 DR HSSP; P11362; IFCK.
 DR Interpro; IPR000719; Euk_pkinase.
 DR Interpro; IPR002011; Receptor_Tyr_Kin_II.
 DR Interpro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;
 KW Transmembrane; Tyrosine-protein kinase.
 SO SEQUENCE 503 AA; 58174 MW; 17273FF47557E2FD CRC64;

Query Match 12.5%; Score 615; DB 4; Length 503;
 Best Local Similarity 45.2%; Pred. No. 1.4e-40;
 Matches 138; Conservative 45; Mismatches 86; Indels 36; Gaps 9;

OY 607 RSRLRFKELGEGQFGEVHLCYDVS---PQDLVSLDPLNVRKGHPLVAVKILRPDATK 663
 DB 214 RDIIVAKMLGEGAFKQVFLAECHNLPLEPD-----KMLVAVK-----ALK 254
 OY 664 NASESLFSRNDFLEKVKINSRLKDPNIRLLGVQVDDPLCMITDMENGDNLNOLSAHO 723
 DB 255 EASES--ANQDQREAEELLTMLOHIVFFGCTEGRPLLMVFEMRGDRLRFLRSIG 312
 OY 724 LEDKAEGAPGQGAQGGTISYPMILHVAAGIASGRIATLNFVHRDLATRNCLVGEN 783
 DB 313 PDKKLAGE--DVAPGP-LGIGQLLAVASOVAAGMVTLAGLHFVHRDLATRNCLVGOG 368
 OY 784 FTIKIDFGMSRNLVAGDYRYVQGRAVLPIRMAMECIIMKFTTASDVMAFGVTLMEV 843
 DB 369 LVYKIDFGMSNDIYTDVYRGGRTMLPIRMMPRESILYRKFTTESDVMSFGVTLMEI 428
 OY 844 MLCRAQPGQLTDEQVLENAGEFFPDGROYLLSRPPACPOGLYELMLRCMSRESEORP 903
 DB 429 TYGK-QPWFQLSNTEAIDCI-----TQGR-VLEPRACPREYVAIMRGCMQREPOQRS 480
 OY 904 FSQLH 908
 DB 481 IKDVH 485

Mon Oct 7 15:50:49 2002

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Job time: 285 sec